

<!--StartFragment-->RESULT 1

ADC00348

ID ADC00348 standard; protein; 441 AA.

XX

AC ADC00348;

XX

DT 15-JUN-2007 (revised)

DT 04-DEC-2003 (first entry)

XX

DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 393.

XX

KW enterohaemorrhagic; anti-bacterial; BOND_PC; hypothetical protein;

KW hypothetical protein ECs1812 [Escherichia coli O157:H7];

KW hypothetical protein ECs1812 [Escherichia coli O157:H7 str. Sakai];

KW unknown protein encoded by cryptic prophage CP-933P;

KW hypothetical protein [Escherichia coli O157:H7 str. Sakai].

XX

OS Escherichia coli; O157:H7.

XX

PN JP2002355074-A.

XX

PD 10-DEC-2002.

XX

PF 24-JAN-2002; 2002JP-00015959.

XX

PR 24-JAN-2001; 2001JP-00112010.

XX

PA (UYTS-) UNIV TSUKUBA.

XX

DR WPI; 2003-451640/43.

DR PC:NCBI; gi|3259568.

XX

PT Enterohemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule

PT and a polypeptide and its use, a polypeptide, a vector and a host cell.

XX

PS Claim 3; SEQ ID NO 393; 2067pp; Japanese.

XX

CC The invention relates to a novel enterohaemorrhagic Escherichia coli

CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention

CC has anti-bacterial activity. The polypeptide can be used in detection

CC and/or treatment of O157:H7 infection. The nucleotide sequence of the

CC genome of Enterohaemorrhagic E. coli O157:H7 was determined. The present

CC sequence represents an E. coli O157:H7-specific polypeptide of the

CC invention.

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed

CC information from BOND.

XX

SQ Sequence 441 AA;

Query Match 100.0%; Score 2341; DB 6; Length 441;
 Best Local Similarity 100.0%; Pred. No. 1.1e-197;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVVNIPDDIQQHAPCGET 60
 |||||||
 Db 1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVVNIPDDIQQHAPCGET 60

Qy 61 TALLSLIKDKGLLGLDEYIAPHLEEGSIGKKTLMFGLFNVTQMALEIPSSVSGISGKY 120
 |||||||
 Db 61 TALLSLIKDKGLLGLDEYIAPHLEEGSIGKKTLMFGLFNVTQMALEIPSSVSGISGKY 120

Qy 121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTAVSTIAST 180
 |||||||
 Db 121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTAVSTIAST 180

Qy 181 GTSATTSTVTTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY 240

APPENDIX A: ALIGNMENT WITH SEQ ID NO 24

APPENDIX B: SEQ ID NO: 24

Db 181 GTSATTSTVTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY 240
|||
Qy 241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLNDNPNTKYAVLTNAAANALGALGGF 300
|||
Db 241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLNDNPNTKYAVLTNAAANALGALGGF 300
|||
Qy 301 AVSRFASTDPMSPHIGAMVGQAAGHAIQYNTPGLKPDTILWWAGATLGAADLNKAEEFV 360
|||
Db 301 AVSRFASTDPMSPHIGAMVGQAAGHAIQYNTPGLKPDTILWWAGATLGAADLNKAEEFV 360
|||
Qy 361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
|||
Db 361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
|||
Qy 421 LPHHNPSNHVDIFDIIQETRV 441
|||
Db 421 LPHHNPSNHVDIFDIIQETRV 441
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